CLAIMS

What is claimed is:

- 1. A method of modulating angiogenesis at a site, the method comprising causing an effective amount of a composition comprising a BTL.012-like protein to be supplied to the site.
- 2. The method of claim 1 wherein the BTL.012-like protein has an amino acid sequence identical to SEQ ID NO:1.
- 3. The method of claim 1 wherein the BTL.012-like protein has an amino acid sequence which is at least 60% identical over at least 40 residues to SEQ ID NO:1.
- 4. The method of claim 1 wherein the BTL.012-like protein has an amino acid sequence which is at least 70% identical over at least 30 residues to SEQ ID NO:1.
- 5. A method of modulating the formation of cells into capillary-like structures comprising contacting the cells with a biologically effective amount of a composition comprising a BTL.012-like protein.
- 6. The method of claim 5 wherein the cells are endothelial cells of human origin.
- 7. A protein characterized by having a deduced amino acid sequence which is at least 60% identical over 40 residues to SEQ ID NO:1.
- 8. The protein according to claim 7, wherein the deduced amino acid sequence is at least 80% identical over 50 residues to SEQ ID NO:1.

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9. A pharmaceutical composition for modulating angiogenesis comprising a protein characterized by having a deduced amino acid sequence which is at least 60% identical over 40 residues to SEQ ID NO:1 and a pharmaceutically acceptable carrier.

- 10. The method of claim 1, wherein the site is within a human patient and the protein is supplied to the site via a pharmaceutical composition according to claim 9.
- 11. The method of claim 10, wherein the site is within a human patient and the protein is supplied to the site via a process of gene therapy.
- 12. A method for preventing, treating, or ameliorating a medical condition in an individual, the method comprising providing a source of an effective amount of at least one protein according to claim 7 to the individual.
- 13. The method of claim 12, wherein the protein is supplied to the individual by providing to the individual a source of a polynucleotide encoding the protein and expressing the protein in vivo.
- 14. The method of claim 12, wherein the medical condition is selected from the group consisting of cancer, metastasis, diabetic retinopathy, macular degeneration, cardiovascular disease, and a wound.
- 15. A polynucleotide selected from the group consisting of (a) a polynucleotide coding for a protein according to claim 7; (b) a polynucleotide complementary to (a); (c) a polynucleotide having at least 90% identity over at least 20 bases to SEQ ID NO:34; and (d) a polynucleotide complementary to (c).

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16. The polynucleotide according to claim 15, wherein the polynucleotide is operably linked within an expression vector to a promoter, the expression vector thus being capable of being used to express the protein according to claim 1.

- 17. A method for producing a protein according to claim 7 comprising the steps of
- (a) introducing an expression vector capable of expressing the protein according to claim 7 into a cell capable of expressing the protein according to claim 7,
- (b) growing cells resulting from step (a) under conditions sufficient to allow the cells to express the protein according to claim 7, and
- (c) recovering the protein according to claim 7 from the result of step (b).
- 18. An antibody against a protein according to claim 7.
- 19. A method for diagnosing a disease or medical condition or susceptibility to a disease or medical condition, the disease or medical condition related to inadequate or excess expression of a protein according to claim 7, the method comprising the steps
 - (a) determining the level of expression of said protein in a sample; and
- (b) comparing the level of expression of said protein against a standard to make a diagnosis.
- 20. The method of claim 19, wherein the medical condition is selected from the group consisting of cancer, metastasis, diabetic retinopathy, macular degeneration, cardiovascular disease, and a wound.
- 21. A protein characterized by having a deduced amino acid sequence which is at least 60% identical over 40 residues to SEQ ID NO:33.